

mountainous parts in the western cordilleras. Species are presently found from Mexico to Central America and the Caribbean south to the Andes from Venezuela to northern Argentina. The history of the classification of the Liabeae reflects the difficulty in tribal placement encountered by early workers. CASSINI, LESSING, DE CANDOLLE, WEDDELL, and BENTHAM and HOOKER all variously treated groups of taxa that are now placed in this tribe but they were not grouped together. RYDBERG formally proposed tribal status in 1927. BENTHAM's classification, which placed the majority of taxa in one genus, *Liabum*, in the Senecionieae, was essentially adopted by HOFFMANN, and despite the work by RYDBERG, was retained more or less intact and accepted by many modern workers. In the 1970's ROBINSON and co-workers published a series of papers bringing the genera together into one tribe and ROBINSON provided the first modern view of the tribe. Previously published phylogenies of the tribe along with a newly generated one based on molecular data from a study by KIM and FUNK show that of the three subtribes, only two are monophyletic. The Paranepheleinae (*Paranepheleus* and *Pseudonoseris*) is monophyletic. The Munnoziinae is most likely monophyletic, although *Chrysactinium* is nested within *Munnozia*. Some core element of the Liabinae is monophyletic but the placement of the smaller genera is in question (e.g., *Cacosmia*, *Chionopappus*). The tribe is primarily Andean, however there have been two independent major invasions northward, viz. *Liabum* from the Andes to Mexico, Central America and the West Indies, and the *Sinclairia* – *Liabellum* clade from the Andes to Mexico and Central America. On the species level, the majority of the diversity is found in the central Andes from southern Colombia to northern Bolivia; on the generic level diversity is concentrated in Ecuador and northern Peru. Speciation patterns seem to support allopatric speciation via peripheral isolation.

Reconstruction of the phylogeny of the Lactuceae (Asteraceae) using the internal transcribed spacer regions ITS 1 + 2

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The tribe Lactuceae, subfamily Cichorioideae, comprises 11 subtribes and 98 genera. We have amplified and sequenced the internal transcribed spacers ITS1 and ITS2 of the ribosomal RNA from more than 100 species and analysed these together with 40 sequences from Genebank, altogether representing 44 genera, covering all subtribes. An unambiguous alignment of these spacer regions across the Lactuceae is

impossible in some parts, however sufficient conserved sequence motifs can be recognized for a valid comparison resulting in a well resolved phylogeny.

The monophyly of the subtribes Sonchinae, Crepidinae, Lactucinae, Hypochaeridinae and Hieraciinae cannot be confirmed and the subtribal status of several genera (e.g. *Cichorium*, *Chondrilla*, *Hyoseris*, *Prenanthes*, *Rhagadiolus*, *Scolymus*, *Taeckholmia*, *Tolpis*, *Urospermum*) need to be revised.

One likely source of error in ITS phylogenies is the fact that in allopolyploid and even diploid hybrids ITS sequences may get recombined and homogenized by concerted evolution. Due to the tree like structure of phylogenetic reconstructions, hybrids then predominantly cluster basal to both or near one of the two parents. This, however, doesn't always reflect their true evolutionary relationship and may lead to wrong phylogenetic implications. To avoid misleading conclusions chromosome counts of the taxa included in this analysis have been carried out and polyploid taxa were excluded from the analysis.

The systematic study of *Achillea* species (Compositae–Anthemideae) in Iran

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The genus *Achillea* L. belongs to the tribe Anthemideae and is one of the larger genera of the family Asteraceae in Iran. Altogether the genus includes 100 species distributed all over the world. There are 15 species that have been studied in this work, of which 7 species are endemic in Iran. They are perennial plants with many medicinal applications. The main objective of this research is study of the species of the genus *Achillea* using numerical taxonomic methods. 63 characters of morphological studies (quantitative and qualitative) of samples were recorded. These data were analysed and interpreted by the JMP, software and cluster analysis (using Ward method). The results of cluster analysis dendrogram confirm classic taxonomic studies. The taxa of *Achillea* that have been studied in this work are as follows: *A. biebersteinii*, *conferta*, *eriphora*, *filiopendulina*, *kellalensis*, *millefolium*, *nobilis*, *oligocephala*, *oxydonta*, *pachycephala*, *setacea*, *talagonica*, *tenuifolia*, *vermicularis* and *wilhelmsii*.